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agcatccacca agacgatcc caagagccaa gttttctta aatgtaaacag ctgtccaaatc 720
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<210> 357

<211> 1536

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<213> Artificial Sequence

<220>

<223> fusion polynucleotide

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<211> 1696

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 358

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<212> PRT

<213> Artificial Sequence

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<223> fusion polypeptide

<400> 359

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Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu	35	40	45	
Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu	50	55	60	
Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala	65	70	75	80
Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys Ser Gln	85	90	95	
Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala Ile Tyr	100	105	110	
Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Ala Met	115	120	125	
Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser	130	135	140	

<210> 360

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 360

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Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu	35	40	45	
Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala Ala Phe Ile	50	55	60	
Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys Ser Gln Val Phe Phe	65	70	75	80
Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala Ile Tyr Tyr Cys Ala	85	90	95	
Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Ala Met Asp Tyr Trp	100	105	110	
Gly Gln Gly Thr Ser Val Thr Val Ser Ser				

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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120

<210> 361
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 361
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20 25 30
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
50 55 60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65 70 75 80
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
85 90 95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125
Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Ser Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
145 150 155 160
Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
165 170 175
Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
180 185 190
Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
195 200 205

<210> 362
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 362
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
1 5 10 15
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
20 25 30
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
50 55 60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65 70 75 80
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
85 90 95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125
Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Ser Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
145 150 155 160
Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
165 170 175
Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
180 185 190
Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
195 200 205

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys
210 215 220
Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala
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Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr
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<210> 363
<211> 505
<212> PRT
<213> Artificial sequence

<220>
<223> fusion polypeptide

<400> 363
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20 25 30
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
50 55 60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65 70 75 80
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
85 90 95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125
Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
145 150 155 160
Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
165 170 175
Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
180 185 190
Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
195 200 205
Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys
210 215 220
Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala
225 230 235 240
Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr
245 250 255
Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp
260 265 270
Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
275 280 285
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
290 295 300
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
305 310 315 320
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
325 330 335
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
340 345 350
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
355 360 365
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
370 375 380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 405 405 410 415
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 420 420 425 430
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 435 435 440 445
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 450 455 460
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
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 485 490 495
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<210> 364

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 364

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 Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
 35 35 40 45
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 50 50 55 60
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
 65 65 70 75 80
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 85 85 90 95
 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 100 100 105 110
 Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
 115 115 120 125
 Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly
 130 130 135 140
 Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
 145 145 150 155 160
 Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
 165 165 170 175
 Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
 180 180 185 190
 Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
 195 195 200 205
 Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys
 210 210 215 220
 Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala
 225 225 230 235 240
 Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr
 245 245 250 255
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp
 260 260 265 270
 Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 275 275 280 285
 Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys
 290 290 295 300
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 305 305 310 315 320
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 325 325 330 335

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
370 375 380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
385 390 395 400
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
405 410 415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
420 425 430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
435 440 445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
450 455 460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
465 470 475 480
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
485 490 495
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu
500 505 510
Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile
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<210> 365

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to introduce mutation in CH3 at position
405 XX to Y

<400> 365

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gtagaaggag cc 72

<210> 366

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to introduce mutation in CH3 at position
405 XX to A

<400> 366

gttgttgaag acgttccct gctgccacct gctcttgccc acggtagct tgctgttagag 60
ggcgaaggag cc 72

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<211> 72

<212> DNA

<213> Artificial Sequence

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<223> 3' oligo to introduce mutation in CH3 at position
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<400> 367

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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405 XX to Y and 407 to A

<400> 368
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<210> 369
<211> 72
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<223> 3' oligo to introduce mutation in CH3 at position
405 XX to A and 407 to Y

<400> 369
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<210> 370
<211> 324
<212> DNA
<213> Artificial Sequence

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tgggagagca atgggcagcc ggagaacaac tacaagacca cgccctccgt gctgtaccc 180
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tgggagagca atgggcagcc ggagaacaac tacaagacca cgccctccgt gctgtaccc 180
gacggctctt tccggctcta tagcaagctc accgtggaca agagcagggt gcagcagggg 240
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cttcctctgt ccccggttaa atga 324

<210> 372
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<212> DNA
<213> Artificial Sequence

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>
<223> fusion polynucleotide

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tggagagaca atgggcagcc ggagaacaaac tacaagacca cgcccccgt gctggactcc 180
gacggctctc tcttcctcgc cagaacgctc accgtggaca agagcaggta gcacggggg 240
aacgtttctc catgtcccgat gatgcattgg gctctgcaca accactacac gcagaagagc 300
cttcgggtaa atgaa 324
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<210> 373

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<213> Artificial Sequence

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<400> 373

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tggagagaca atgggcagcc ggagaacaaac tacaagacca cgcccccgt gctggactcc 180
gacggctctc tcttcctcgc cagaacgctc accgtggaca agagcaggta gcacggggg 240
aacgtttctc catgtcccgat gatgcattgg gctctgcaca accactacac gcagaagagc 300
cttcgggtaa atgaa 324
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<210> 374

<211> 324

<212> DNA

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<223> fusion polynucleotide

<400> 374

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tggagagaca atgggcagcc ggagaacaaac tacaagacca cgcccccgt gctggactcc 180
gacggctctc tcttcctcgc cagaacgctc accgtggaca agagcaggta gcacggggg 240
aacgtttctc catgtcccgat gatgcattgg gctctgcaca accactacac gcagaagagc 300
cttcgggtaa atgaa 324
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<210> 375

<211> 107

<212> PRT

<213> Artificial Sequence

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<223> fusion polypeptide

<400> 375

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								20			25		30		
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
				35			40			45					
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
				50			55			60					
Tyr	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
				65			70			75			80		
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				85				90				95			

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 376
<211> 107
<212> PRT
<213> Artificial Sequence
<220>
<223> fusion polypeptide

<400> 376
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20 25 30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60
Ala Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 377
<211> 107
<212> PRT
<213> Artificial Sequence
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<400> 377
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60
Phe Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 378
<211> 107
<212> PRT
<213> Artificial Sequence
<220>
<223> fusion polypeptide

<400> 378
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

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 20          25          30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 35          40          45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 50          55          60
Tyr Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 65          70          75          80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 85          90          95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100          105

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<210> 379
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 379
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 1 5 10 15
 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 20 25 30
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 35 40 45
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 50 55 60
 Ala Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 65 70 75 80
 Asn Val Phe Ser Cys Ser Val Met His Gln Ala Leu His Asn His Tyr
 85 90 95
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 100 105

<210> 380
<211> 1515
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

2000, February, 2000, 2000

WO 2005/037989

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<210> 381

<211> 1521

<212>

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 381

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caggggggaa	aggtcacaat	gacttgcgg	ggccatgtca	catgcgttt	180	
tatccaggaa	aggcaggatc	ttccccccaa	ccctggatgt	atgcggccat	240	
ttggggagtcc	ctgtcgctt	cagtggcgt	gggttgcgtt	ccttcatact	300	
acggatgggt	gtgtcggtt	tgctgcggc	tatatacgct	atgcgttgaa	360	
ccccacgttc	glgtctggaa	tcataatgc	ctggaaatgg	ggcggtgttc	420	
ggatgggggg	gagggtgggg	tcataatgc	tttttttttt	tgaggatgtg	480	
aggcttttttt	cttcctgggg	tttttttttt	tttttttttt	agtttttttt	540	
aatatgttttt	gttcgttttt	tttttttttt	tttttttttt	atgttttttt	600	
atgtttttttt	gttttttttt	tttttttttt	tttttttttt	atgttttttt	660	
ccgggggggg	gttttttttt	tttttttttt	tttttttttt	atgttttttt	720	
gacaaatccct	gttttttttt	tttttttttt	tttttttttt	atgttttttt	780	
ttttttttttt	gttttttttt	tttttttttt	tttttttttt	atgttttttt	840	
ggccgggggg	gttttttttt	tttttttttt	tttttttttt	atgttttttt	900	
ccccatccca	gttttttttt	tttttttttt	tttttttttt	atgttttttt	960	
ccccccaaaa	gttttttttt	tttttttttt	tttttttttt	atgttttttt	1020	
gggggggggg	gttttttttt	tttttttttt	tttttttttt	atgttttttt	1080	
gttggatccgg	gttttttttt	tttttttttt	tttttttttt	atgttttttt	1140	
gttgcataatg	gttttttttt	tttttttttt	tttttttttt	atgttttttt	1200	
gggggggggg	gttttttttt	tttttttttt	tttttttttt	atgttttttt	1260	
gggggggggg	gttttttttt	tttttttttt	tttttttttt	atgttttttt	1320	
gggggggggg	gttttttttt	tttttttttt	tttttttttt	atgttttttt	1380	
gggggggggg	gttttttttt	tttttttttt	tttttttttt	atgttttttt	1440	
gggggggggg	gttttttttt	tttttttttt	tttttttttt	atgttttttt	1500	
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<210> 382

<211> 1515

<212>

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 382

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ccaggggaga  aggtttccat  gacttgcggg  ggccatgtcaa  gtgttgcgtt  catgcatgcg 180
taccggccat  ggccaggatc  tcctcccaaa  ctgttttttttt  atgcggccat  caactgtgt 240
ttttggatcc  ctgttcgttt  ctgttttttttt  ctgttttttttt  cttttttttttt  ttttttttttt 300
aggcaggatgg  aggttttttt  tcgttttttttt  tcgttttttttt  tcgttttttttt  tcgttttttttt 360
cccaatccat  gtgttttttt  tcgttttttttt  tcgttttttttt  tcgttttttttt  tcgttttttttt 420
ggatctttgg  gggttttttt  tcgttttttttt  tcgttttttttt  tcgttttttttt  tcgttttttttt 480
aggcttttttt  ctcgtttttt  tcgttttttttt  tcgttttttttt  tcgttttttttt  tcgttttttttt 540
aatatgttc  ggtttttttt  tcgttttttttt  tcgttttttttt  tcgttttttttt  tcgttttttttt 600
ccaggatccat  gtgttttttt  tcgttttttttt  tcgttttttttt  tcgttttttttt  tcgttttttttt 660
gaaatccat  ccacggacac  tcataatgttc  atttttcgcgt  tcctgtcaat  cagtgttc 720

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<210> 383

<211> 1515

<212>

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 383

<210> 384

<211> 1515

<212> 1

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 384

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Ccaggggaga aatgtccat gactgtcagg ggccatgtcaa gtgttggat tgcgtatgg 180
taccacaga agccaggatc cttcccaaaat ggttggatgtt atgcggccatc caactcggt 240
ttggatgttc ctgtctggatc cttttttttt ggtttttttt cttttttttt ttcgtttttt 300

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<210> 385
<211> 500

<212> PRT

<220>
<223> fusion polypeptide

<400> 385
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 val Ile Ile Ala Arg Gly Gln Ile val 10 Leu Ser Gln Ser Pro Ala Ile
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 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Gln Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser 225 Leu Thr Ser Gln Asp Ser Ala Val Tyr Phe Cys
 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285

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 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Glu Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Glu Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys 500

<210> 386

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 386
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 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220

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 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Tyr Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
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<210> 387

<211> 500

<212> PRT

<213> Artificial sequence

<220>

<223> fusion polypeptide

<400> 387

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160

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 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Gly Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Val Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Ala Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
 500

<210> 388

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 388

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95

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 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser ser ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Tyr Leu Ala Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys 500

<210> 389

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 389

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30

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 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asp Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Ala Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys 500

<210> 390

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' oligo to mutat IgG1

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tctccggta aatgatctag a 1521

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 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> fusion polynucleotide

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 ccaggggaga aggtccaaat gacttgcagg gccagctcaa gtgtaaagttt catgcactgg 180
 taccagcaga agccggatcc ttcccccggaa ccttggatatt atgccccatc caacctggct 240
 tctggatgtcc ctgtctgtt cagttgcagg tggtttggggaa cttcttacttc ttccacaatc 300
 agcagatgtcc aggttgcggaa tgctgttgcact tttttactgcg agcagtggggat tttaaaccctt 360
 cccacatgtcc gtgtttgggg ccaggatgtt ctgtttttttt gggccgtgtt gggccgtgtt 420
 ggatcttgggg ggggttgggg ctcttcaggct tttttttttt gggccgtgtt tgactgtgg 480
 aggccctgggg ctttcgtgtt gatgttcttc aagggtttctg gttttttttt taccatgtt 540
 aatatgtccat ggttttttttccaaatccatc gatccatgtt gggggccgttgg aatggatttttt 600
 ccaggaaatgtt gtttttttttccatcataatccatc aatgttcaatgg gcaaggccatc actgtactttt 660
 gacaaaatccat ccaggacatcc ttccatgttcc aatgttcaatgg gcaaggccatc actgtactttt 720
 gtcttatttttccatc aatgttcaatgg ggttttttttccatcataatccatc aatgttcaatgg gcaaggccatc actgtactttt 780
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<210> 395
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 <223> fusion polynucleotide

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<210> 396

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 396

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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35          40          45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Lys Pro Gly Ser Ser
 50          55          60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65          70          75          80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85          90          95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100          105          110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115          120          125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130          135          140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145          150          155          160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165          170          175
Asn Met His Trp Val Lys Gln Thr pro Arg Gln Gly Leu Glu Trp Ile
180          185          190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195          200          205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
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225          230          235          240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245          250          255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
260          265          270
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
275          280          285
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
290          295          300
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305          310          315          320
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
325          330          335
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
340          345          350
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
355          360          365
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
370          375          380
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

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405 410 415
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 425 430 435
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
440 445
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480
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485 490 495
Ser Pro Gly Lys 500

<210> 397
<211> 500
<212> PRT
<213> Artificial sequence

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<223> fusion polypeptide

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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
260 265 270
Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro Ala Pro Glu Leu Leu
275 280 285
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
290 295 300
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305 310 315 320
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

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 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
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 485 490 495
 Ser Pro Gly Lys 500

<210> 398

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 398

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 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
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 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
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 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Glu Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
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<210> 400
 <211> 264
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 35 40 45
 Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro
 50 55 60
 Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser
 65 70 75 80
 Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn
 85 90 95
 Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg
 100 105 110
 Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg
 115 120 125
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
 130 135 140
 Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys Pro Gly Ala Ser
 145 150 155 160
 Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe Thr Asp His Tyr
 165 170 175
 Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu Gln Trp Ile Gly
 180 185 190
 Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Gln
 195 200 205
 Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser Thr Ala Tyr Met
 210 215 220
 Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala
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<210> 401

<211> 36

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<213> Artificial sequence

<220>

<223> oligonucleotide primer

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<211> 44

<212> DNA

<213> Artificial sequence

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<400> 402

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<210> 403

<211> 47

<212> DNA

<213> Artificial sequence

<220>

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<213> Artificial Sequence
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<211> 48
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<223> oligonucleotide primer

<400> 405
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<223> oligonucleotide

<400> 406
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caaggatgttcc acgaggcccg tgaccctccat aacaggatgtt gggccatgtt cccgtgttca 600
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<210> 408

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<223> fusion polypeptide<400> 408
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35 40 45
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu
50 55 60
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg
65 70 75 80
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly
85 90 95
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly
100 105 110
Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys
115 120 125
Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val
130 135 140
Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr
145 150 155 160
Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val
165 170 175
Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg
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<211> 60
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<220>
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<400> 414
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<400> 415
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<400> 416
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<211> 645
<212> DNA
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<220>
<223> fusion polynucleotide

<400> 417

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<211> 210

<212> PRT

<213> Artificial Sequence

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<223> fusion polypeptide

<400> 418

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 35 40 45
 Asp Leu Phe Thr Val Leu Leu Glu Gln Asn Asp Leu Glu Arg Gly His
 50 55 60
 Thr Gly Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu
 65 70 75 80
 Leu Gln Arg Leu Asp Asp Phe Glu Ala Gly Thr Ala Thr Ala Ala Pro
 85 90 95
 Pro Gly Glu Ala Asp Leu Gln Val Ala Phe Asp Ile Val Cys Asp Asn
 100 105 110
 Val Gly Arg Asp Trp Lys Arg Leu Ala Arg Glu Leu Lys Val Ser Glu
 115 120 125
 Ala Lys Met Asp Gly Ile Glu Lys Tyr Pro Arg Ser Leu Ser Glu
 130 135 140
 Arg Val Arg Glu Ser Leu Lys Val Trp Lys Asn Ala Glu Lys Lys Asn
 145 150 155 160
 Ala Ser Val Ala Gly Leu Val Lys Ala Leu Arg Thr Cys Arg Leu Asn
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